WE CLAIM:

1. An isolated polynucleotide from coryneform bacteria, containing a polynucleotide sequence coding for the sigM gene, selected from the group consisting of:

   a) a polynucleotide that is at least 70% identical with a polynucleotide that codes for a polypeptide containing the amino acid sequence of SEQ ID No. 2,

   b) a polynucleotide that codes for a polypeptide containing an amino acid sequence that is at least 70% identical with the amino acid sequence of SEQ ID No. 2,

   c) a polynucleotide that is complementary to the polynucleotides of a) or b), and

   d) a polynucleotide containing at least 15 consecutive nucleotides of the polynucleotide sequence of a), b) or c).

2. The polynucleotide according to claim 1, wherein the polypeptide has sigma factor M activity.

3. The polynucleotide according to claim 1, wherein the polynucleotide is a recombinant DNA, that is replicable in coryneform bacteria.

4. The polynucleotide according to claim 1, wherein the polynucleotide is an RNA.

5. The polynucleotide according to claim 3, comprising the nucleic acid sequence as shown in SEQ ID No. 1.

6. The polynucleotide according to claim 3, wherein the DNA, comprises

   (i) the nucleotide sequence shown in SEQ ID No. 1, or

(ii) at least one sequence that corresponds to sequence (i) within the region of the degeneracy of the genetic code, or

(iii) at least one sequence that hybridizes with the sequence that is complementary to sequence (i) or (ii).

7. The polynucleotide according to claim 6, further comprising

(iv) sense mutations in (i) that are neutral in terms of function.

8. The polynucleotide according to claim 6, wherein the hybridization of sequence (iii) is carried out under conditions of stringency corresponding at most to 2x SSC.

9. The polynucleotide sequence according to claim 3, which codes for a polypeptide containing the amino acid sequence shown in SEQ ID No. 2.

10. A Coryneform bacterium in which the sigM gene is enhanced.

11. A Coryneform bacterium in which the sigM gene is overexpressed.

12. An Escherichia coli strain DH5amcr/pEC-XK99EsigMa1ex deposited as DSM 14409.

13. A method for the production of L-amino acids in coryneform bacteria, comprising:

a) fermenting, in a medium, the coryneform bacteria producing the desired L-amino acid, in which bacteria at least the endogenous sigM gene or nucleotide sequences coding therefor are enhanced.

14. The method according to claim 13, further comprising:

    b) concentrating the L-amino acid in the medium or in the cells of the bacteria.

15. The method according to claim 14, further comprising:

    c) isolating the L-amino acid.

16. The method according to claim 13, wherein the L amino acids are lysine.

17. The method according to claim 13, wherein at least the sigM gene or nucleotide sequences coding for the latter are overexpressed.

18. The method according to claim 13, wherein additional genes of the biosynthesis pathway of the desired L-amino acid are enhanced in the bacteria.

19. The method according to claim 13, wherein bacteria are used in which at least some of the metabolic pathways that reduce formation of the desired L-amino acid are excluded.

20. The method according to claim 13, wherein a strain transformed by a plasmid vector is used, and the plasmid vector carries the nucleotide sequence coding for the sigM gene.

21. The method according to claim 13, wherein expression of the polynucleotide(s) coding for the sigM gene is enhanced.

22. The method according to claim 13, wherein expression of the polynucleotide(s) coding for the sigM gene is overexpressed.

23. The method according to claim 13, wherein the regulatory properties of the polypeptide for which the polynucleotide sigM codes are increased.

24. The method according to claim 13, wherein the bacteria being fermented comprise, at the same time, one or more genes which are enhanced or overexpressed; wherein the one or more genes is/are selected from the group consisting of:

the gene dapA coding for dihydrodipicolinate synthase,

the gene gap coding for glyceraldehyde-3-phosphate dehydrogenase,

the gene tpi coding for triose phosphate isomerase,

the gene pgk coding for 3-phosphoglycerate kinase,

the gene zwf coding for glucose-6-phosphate dehydrogenase,

the gene pyc coding for pyruvate carboxylase,

the gene mqo coding for malate quinone oxidoreductase,

the gene lysC coding for a feed-back resistant aspartate kinase,

the gene lysE coding for lysine export,

the gene hom coding for homoserine dehydrogenase,

the gene ilvA coding for threonine dehydratase or the allele ilvA(Fbr) coding for a feed-back resistant threonine dehydratase,

the gene ilvBN coding for acetohydroxy acid synthase,

the gene ilvD coding for dihydroxy acid dehydratase, and

the gene zwa1 coding for the Zwa1 protein.

25. The method according to claim 13, wherein the bacteria being fermented comprise, at the same time, one or more genes which are attenuated; wherein the one or more genes is/are selected from the group consisting of:

the gene pck coding for phosphoenol pyruvate carboxykinase,

the gene pgi coding for glucose-6-phosphate isomerase,

the gene poxB coding for pyruvate oxidase, and

the gene zwa2 coding for the Zwa2 protein.

26. The method according to claim 13, wherein microorganisms of the genus Corynebacterium are used.

27. The method according to claim 26, wherein the Corynebacterium glutamicum strain DSM5715/pEC-XK99EsigMa1ex is used.

28. A Coryneform bacterium comprising a vector that carries a polynucleotide according to claim 1.

29. A method of finding RNA, cDNA and DNA in order to isolate nucleic acids, or polynucleotides or genes, that code for sigma factor M or are very similar to the sequence of the sigM gene, which method comprises comprising contacting the RNA, cDNA, or DNA with hybridization probes comprising polynucleotide sequences according to claim 1.

30. The method according to claim 29, wherein arrays, micro arrays or DNA chips are used.